

JA



PCT09

## RAW SEQUENCE LISTING

DATE: 02/13/2002

PATENT APPLICATION: US/09/889,926

TIME: 07:25:06

Input Set : A:\2248-115.app

Output Set: N:\CRF3\02132002\I889926.raw

ENTERED

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3 <110> APPLICANT: Xie, Qi
4      Chua, Nam-Hai
5      Institute of Molecular Agrobiolgy, The National U
7 <120> TITLE OF INVENTION: NAC1 - A PLANT GENE ENCODING A TRANSCRIPTION FACTOR
8      INVOLVED IN COTYLEDON AND LATERAL ROOT DEVELOPMENT
10 <130> FILE REFERENCE: 2248-115
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/889,926
C--> 13 <141> CURRENT FILING DATE: 2001-08-18
15 <160> NUMBER OF SEQ ID NOS: 2
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1287
21 <212> TYPE: DNA
22 <213> ORGANISM: Arabidopsis thaliana
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31 aaaacctaga aaaaaaaagg atcaaatc atg gag acg gaa gaa gag atg aag 112
32                               Met Glu Thr Glu Glu Glu Met Lys
33                               1           5
35 gaa agt agt ata agc atg gtg gag gca aag ttg cct ccg gga ttc aga 160
36 Glu Ser Ser Ile Ser Met Val Glu Ala Lys Leu Pro Pro Gly Phe Arg
37   10           15           20
39 ttt cac ccg aag gac gat gag ctt gtc tgc gat tac ttg atg aga cga 208
40 Phe His Pro Lys Asp Asp Glu Leu Val Cys Asp Tyr Leu Met Arg Arg
41 25           30           35           40
43 tcg ctt cac aat aat cat cga cca cct ctt gtc ctg atc caa gtc gat 256
44 Ser Leu His Asn Asn His Arg Pro Pro Leu Val Leu Ile Gln Val Asp
45           45           50           55
47 ctc aac aag tgt gag cct tgg gac atc cca aaa atg gca tgc gtg gga 304
48 Leu Asn Lys Cys Glu Pro Trp Asp Ile Pro Lys Met Ala Cys Val Gly
49           60           65           70
51 ggg aag gat tgg tat ttc tac agc caa aga gac cga aaa tac gcg acg 352
52 Gly Lys Asp Trp Tyr Phe Tyr Ser Gln Arg Asp Arg Lys Tyr Ala Thr
53           75           80           85
55 ggg ctg aga act aac cga gca acg gcc acc gga tat tgg aaa gcc acc 400
56 Gly Leu Arg Thr Asn Arg Ala Thr Ala Thr Gly Tyr Trp Lys Ala Thr
57           90           95           100
59 ggc aaa gac aga acc att cta aga aag ggt aag cta gtt ggg atg agg 448
60 Gly Lys Asp Arg Thr Ile Leu Arg Lys Gly Lys Leu Val Gly Met Arg
61 105           110           115           120

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63 aag aca ttg gtt ttc tat caa ggt cga gct cct cga ggc cgt aaa acc 496
64 Lys Thr Leu Val Phe Tyr Gln Gly Arg Ala Pro Arg Gly Arg Lys Thr
65 125 130 135
67 gat tgg gtc atg cac gaa ttc cgt ctc caa gga tct cat cat cct ccc 544
68 Asp Trp Val Met His Glu Phe Arg Leu Gln Gly Ser His His Pro Pro
69 140 145 150
71 aat cat tct ctg agc tct cca aag gaa gac tgg gtc ttg tgt agg gta 592
72 Asn His Ser Leu Ser Ser Pro Lys Glu Asp Trp Val Leu Cys Arg Val
73 155 160 165
75 ttc cat aag aat acg gaa gga gtt ata tgt aga gac aac atg gga agc 640
76 Phe His Lys Asn Thr Glu Gly Val Ile Cys Arg Asp Asn Met Gly Ser
77 170 175 180
79 tgt ttt gat gag aca gcc tct gca tcg ctt cct cca ctg atg gat cct 688
80 Cys Phe Asp Glu Thr Ala Ser Ala Ser Leu Pro Pro Leu Met Asp Pro
81 185 190 195 200
83 tac atc aac ttt gac caa gaa ccc tct tct tat ctc agt gat gat cat 736
84 Tyr Ile Asn Phe Asp Gln Glu Pro Ser Ser Tyr Leu Ser Asp Asp His
85 205 210 215
87 cac tac atc atc aat gag cac gta ccc tgc ttc tcc aat ttg tca cag 784
88 His Tyr Ile Ile Asn Glu His Val Pro Cys Phe Ser Asn Leu Ser Gln
89 220 225 230
91 aac caa acc tta aac tcg aac cta acc aac tca gtc tct gaa ctc aag 832
92 Asn Gln Thr Leu Asn Ser Asn Leu Thr Asn Ser Val Ser Glu Leu Lys
93 235 240 245
95 att cca tgc aag aac cct aac ccc ttg ttt act ggt ggt tca gcc tca 880
96 Ile Pro Cys Lys Asn Pro Asn Pro Leu Phe Thr Gly Gly Ser Ala Ser
97 250 255 260
99 gcc acg ctc aca ggc ctc gac tca ttc tgt tct tca gat cag atg gtt 928
100 Ala Thr Leu Thr Gly Leu Asp Ser Phe Cys Ser Ser Asp Gln Met Val
101 265 270 275 280
103 ctc aga gct cta ctc agt cag ctc act aag att gat gga agc ctc ggg 976
104 Leu Arg Ala Leu Leu Ser Gln Leu Thr Lys Ile Asp Gly Ser Leu Gly
105 285 290 295
107 cct aaa gaa tca cag agt tat gga gaa ggt agc tcg gag agc ctc ctg 1024
108 Pro Lys Glu Ser Gln Ser Tyr Gly Glu Gly Ser Ser Glu Ser Leu Leu
109 300 305 310
111 acc gac atc ggt att cca agc act gtt tgg aat tgc tgatgatcga 1070
112 Thr Asp Ile Gly Ile Pro Ser Thr Val Trp Asn Cys
113 315 320
115 gtgtaacgag agttactatt gctatatcc tatocatgat tggaacaatt cttcgggggg 1130
117 aaataacgtg tgcttgtctg attgtacaaa catttctca ctcttgtacc cacggtagat 1190
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125 <211> LENGTH: 324
126 <212> TYPE: PRT
127 <213> ORGANISM: Arabidopsis thaliana
129 <400> SEQUENCE: 2
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131      1              5              10              15
133 Ala Lys Leu Pro Pro Gly Phe Arg Phe His Pro Lys Asp Asp Glu Leu
134              20              25              30
136 Val Cys Asp Tyr Leu Met Arg Arg Ser Leu His Asn Asn His Arg Pro
137              35              40              45
139 Pro Leu Val Leu Ile Gln Val Asp Leu Asn Lys Cys Glu Pro Trp Asp
140              50              55              60
142 Ile Pro Lys Met Ala Cys Val Gly Gly Lys Asp Trp Tyr Phe Tyr Ser
143 65              70              75              80
145 Gln Arg Asp Arg Lys Tyr Ala Thr Gly Leu Arg Thr Asn Arg Ala Thr
146              85              90              95
148 Ala Thr Gly Tyr Trp Lys Ala Thr Gly Lys Asp Arg Thr Ile Leu Arg
149              100              105              110
151 Lys Gly Lys Leu Val Gly Met Arg Lys Thr Leu Val Phe Tyr Gln Gly
152              115              120              125
154 Arg Ala Pro Arg Gly Arg Lys Thr Asp Trp Val Met His Glu Phe Arg
155              130              135              140
157 Leu Gln Gly Ser His His Pro Pro Asn His Ser Leu Ser Ser Pro Lys
158 145              150              155              160
160 Glu Asp Trp Val Leu Cys Arg Val Phe His Lys Asn Thr Glu Gly Val
161              165              170              175
163 Ile Cys Arg Asp Asn Met Gly Ser Cys Phe Asp Glu Thr Ala Ser Ala
164              180              185              190
166 Ser Leu Pro Pro Leu Met Asp Pro Tyr Ile Asn Phe Asp Gln Glu Pro
167              195              200              205
169 Ser Ser Tyr Leu Ser Asp Asp His His Tyr Ile Ile Asn Glu His Val
170              210              215              220
172 Pro Cys Phe Ser Asn Leu Ser Gln Asn Gln Thr Leu Asn Ser Asn Leu
173 225              230              235              240
175 Thr Asn Ser Val Ser Glu Leu Lys Ile Pro Cys Lys Asn Pro Asn Pro
176              245              250              255
178 Leu Phe Thr Gly Gly Ser Ala Ser Ala Thr Leu Thr Gly Leu Asp Ser
179              260              265              270
181 Phe Cys Ser Ser Asp Gln Met Val Leu Arg Ala Leu Leu Ser Gln Leu
182              275              280              285
184 Thr Lys Ile Asp Gly Ser Leu Gly Pro Lys Glu Ser Gln Ser Tyr Gly
185              290              295              300
187 Glu Gly Ser Ser Glu Ser Leu Leu Thr Asp Ile Gly Ile Pro Ser Thr
188 305              310              315              320
190 Val Trp Asn Cys

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VERIFICATION SUMMARY

DATE: 02/13/2002

PATENT APPLICATION: US/09/889,926

TIME: 07:25:07

Input Set : A:\2248-115.app

Output Set: N:\CRF3\02132002\I889926.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date